ECORIA

SANTICCGG TGC AGG ACG AAG CTG TTC TGG ATT TCT TAC AGT GAT GGG GAC CAG

Arg Thr Lys Leu Phe Trp lie Ser Tyr Ser Asp Gly Asp Gln

69
TGT GCC TCA AGT CCA TGC CAG AAT GGG GGC TCC TGC AAG GAC CAG CTC CAG TCC
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser

114

129

TAT ATC TGC TTC TGC CTC CCT GCC TTC GAG GGC CGG AAC TGT GAG ACG CAC AAG

Tyr lie Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys

174 189 204 PST IA

GAT GAC CAG CTG ATC TGT GTG AAC GAG AAC GGC GGC TGT GAG CAG TAC TGC AGT

Asp Asp Gln Leu ile Cys Val Asn Glu Asn Gly Gly Gys Glu Gln Tyr Cys Ser

219
234
249
264

GAC CAC ACG GGC ACC AAG CGC TCC TGT CGG TGC CAC GAG GGG TAC TCT CTG CTG

Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu

279

GCA GAC GGG GTG TCC TGC ACA CCC ACA GTT GAA TAT CCA TGT GGA AAA ATA CCT Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro

Xba I 339 354 369
ATT CTA GAA AAA AGA AAT GCC AGC AAA CCC CAA GGC CGA ATT GTG GGG GGC AAG
Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys

384

GTG TGC CCC AAA GGG GAG TGT CCA TGG CAG GTC CTG TTG TTG GTG AAT GGA GCT Val Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala

444
459
474
CAG TTG TGT GGG GGG ACC CTG ATC AAC ACC ATC TGG GTG GTC TCC GCG GCC CAC
Gln Leu Cys Gly Gly Thr Leu lle Asn Thr lle Trp Val Val Ser Ala Ala His

489 504 519 534 TGT TTC GAC AAA ATC AAG AAC TGG AGG AAC CTG ATC GCG GTG CTG GGC GAG CAC Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His

549

GAC CTC AGC GAG CAC GAC GGG GAT GAG CAG AGC CGG CGG GTG GCG CAG GTC ATC

Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val 11e

609 Sma I 624 639

ATC CCC AGC ACG TAC GTC CCG GGC ACC ACC AAC CAC GAC ATC GCG CTG CTC CGC

11e Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp 11e Ala Leu Leu Arg

654

CTG CAC CAG CCC GTG GTC CTC ACT GAC CAT GTG GTG CCC CTC TGC CTG CCC GAA

Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu

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| blygluthrargas bgagaaacacggga | APPROTECTION OF THE PROPERTY O | plyaProg1yf caacoossess | TORI BAT 9 V | TCTTOGTAAC | CAGGAGGAM | COCCACCECE | POCTECACO | | COCAACCOCT | TOCTGGAGGA | CTCCCC |
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| •10 Pro GlySerLeuGl | | •20 | inCvaSari | MaG1uG1uA1 | OE. ArgGluIle | | leGluArgTi | brigeLouPho | TrpIleSer1 | yrSerAspG1 | yAepGln |
| ProGlySerLeuGl CCGGGCTCCCTGG | MAGGGAGTG | CAACGAGGAG | CAGTECTOCT | I COMPONIE | | | | CGAAGCTGTTC 230 | TGGATTTCTT | PACACTEATEC | SGACCAC SEA |
| 250 | 260 | 270 | 260 | 290 | • | | | +80 | ļ. | | |
| +50 CyaAlaSerSerP | roCvaGlpAs | 060 InGlyGlySer | CyalyaAapi | GlnLeuGlnSe | rTyrIleCye | PhoCyalouf | rollaPheG | luGlyArgAss | CyaClaThr | Mi elyelepl e Cacaagga t ga | pGlaLau ccaccac |
| CyaAlaSerSerPo TGTGCCTCAAGTO | CATGOCAGA | TEEGGECTEC | TECANGUNU | | CTATATCT6C 420 | 430 | 440 | 450 | 460 | 470 | 480 |
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| +90 IleCysValAsnG | luAanGlyG | | | AspHisThrG | yThrLyeArg | SerCyeArg | yaHiaGluG | lytyr3erlet cctactctct | CTCCCAGAC | G19Ve1Sercy GGGGTGTOCTG | CACACCC |
| ATCTGTGTGAACG | AGAACGGCE | CTGTGAGCAG | TACTGCAGT 520 | GACCACACEGE 530 | S40 | 550 | 560 | 570 | 500 | 590 | 600 |
| 490 •130 | 500 | 510 +140 | | | -18/ | 0 | | +160 |) | Carrotters. | aValle: |
| 130 ThrvalGluTyrP ACAGTTGAATATO | ToCys61yL | yslieProlle | LouGluLye | ArgaenAleS | or LyaPro Gli | mGlyArgIle Accessatt | alglyglyl Tececece | ACCTCTCCCC | CAMACCCCAC | TETOCATEGO | SCTOCTE |
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| •210 •£luHisAspleui | | +220 | - | V-181-G | •23• 1 1 1 1 1 1 1 1 1 1 1 1 1 | | TvrVelPro | -l-Th-Th-As | n Nie Asolle | Al alculouA | rgioulis |
| GAGCACGACCTC | Serg Lunion ACCGAGCACE | ACCGCGATGA | CAGAGOOG | CECETECCE | AGGTCATCAT | - | | | OCACGACATO | XCCCTCCTCC | SCCTECAC SEO |
| 850 | 860 | 870 | 850 | 630 | -22 | w 220 | | +28 | 0 | | |
| +250 GlnProVelVel | l euThrAsni | +26/ ItaValValPr | | uProGluArgT | | | AlePheVel | ArgPheSerLe | uVelSerGly | /TrpGlyGlnL | euleulep |
| CAGOCCGTGGTO | CTCACTGAC | ATGTGGTGCC | CCTCTGCCT | | OCTTCTCTCA | | | | 1060 | 1070 | 1000 |
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| •290 ArgGlyAleThr CGTGGCGCCACG | 980 AleLeuGlui GCCTGGAGG | 990 +30 Leullet Valle CTCATGGTOCT | 1000 0 wAssValPr CAACGTGCC | oArgLeuHet1 CCGGCTGATG | +31 ThrGlnAspCy ACCCAGGACTE | 10 yalauGlmGlm ccttcCAGCAG | | +32 ValClyAn9e | O rProfenil | eThrGluTyr# | etPheCys |
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| +290 ArgGlyAlaThr CGTGCCGCCACG 1090 +330 | 980 AleLeuGlul GCCCTGGAGG 1100 | 990 +30 LeuBetVelle CTCATGGTCCT 1110 +34 | 1000 WASDVS1Pr CAACGTGCO 1120 | oArgLeuHet1 CCGGCTGATG/ 1130 | +31 ThrGlnAspCy ACCCAGGACTG 1140 +35 | o palauGlmGlm cccrccagcae 1150 | SerArgLys TCACGGAAG 1160 | +82 ValGlyAspSe GTGGGAGACTC 1170 +36 TwrLeuThrGl | O PPTORENTIO CCCARATATO 1180 O VIIOVALSE | oThrGluTyrN CACGGAGTACA 1190 rTrpGlyGluG | etPheCys TGTTCTGT 1200 |
| •290 ArgGlyAleThr CGTEGCGCCACG 1090 •330 AleGlyTyrSer GCCEGCTACTCG | 980 AleLeuGlul GCCCTGGAGG 1100 AspGlySerl GATGGCAGG | 990 +30 Leullet Velle CTCATGGTCCT 1110 +34 LyaAspSerCy AAGGACTCCTG | 1000 QUARDVEIPT CARCETGCO 1120 O PELYREIYAR CARGEGEGA | oArgLeuHet1 CCGGCTGATG/ 1130 | +31 ThrGlnAspCy ACCCAGGACTG 1140 +35 | o palauGlmGlm cccrccagcae 1150 | SerArgLys TCACGGAAG 1160 | +32 ValGlyAspSe GTGGGAGACTO 1170 +36 TyrLauThrGl TACCTGACGGG | O PPPOASNII CCCAAATATI 1180 O VIIOVAISS CATOSTCAG 1300 | aThrGluTyrH CACGGAGTACA 1190 rTrpGlyGlnG CTGGGGCCAGG 1810 | etPheCys TGTTCTGT 1200 |
| •290 ArgGlyAlaThr CCTGCCCCACG 1090 •330 AlaGlyTyrSer CCCGCTACTCG 1210 •370 | \$80 AleLeuGlul GCCCTGGAGG 1100 AspGly3erl GATGGCAGG 1220 | 990 +30 LeulletVelle CTCATGGTCGT 1110 +34 LyaAspSerCy AAGGACTCCTG 1230 +38 | 1000 0 WASDVS1Pr CAACGTGCO 1120 0 MLysG1yAs CAAGGGGGA 1240 | oArgleuHet1 COGGCTGATGI 1180 pSerGlyGlyI CAGTGGAGGC 1250 | +31 ThrG1nAspCy ACCCAGGACTE 1140 +35 ProHisAlsTi CCACATGCCAC 1250 +35 | MALBUGINGING NO STATE OF THE STATE OF T | Serarglys TCACGGAAG 1160 GlyThrTrp GGCACGTGG 1280 | +32 ValGlyAepSe GTGGGAGACTC 1170 +36 TyrLeuThrGl TACCTGACGGC 1290 +46 | O Profession (COCCAMATATO 1180 COCCAMATATO COCCAMATATO COCCATO | eThrGluTyrk caccgagtaca 1190 rTrpGlyGlnG cTGGGGCCAGG 1810 +406 | etPheCys TGTTCTGT 1200 SlyCysAle GCTGCGCA 1320 |
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| •290 ArgGlyAleThr CCTEGCSCCACG 1090 •330 AleGlyTyrSer CCCGGCTACTCG 1210 •370 ThrValGlyHis ACCCTGGCCAC 1330 AGCCCTGGCCTC 1450 CGAGACAGAGAC 1570 GATGGAATAGAC | AleleuGlui GCCCTGAGG 1100 AmpGlySmi GATGGCAGG 1220 PheGlyVel TITIGGGTG 1340 CTGGAGAGAA 1460 CAGAAACAGA 1380 | 990 +90 Leullet Valle CTCATGGTCT 1110 +94 LyaAspSerCy AAGGACTCCTG 1230 +38 TyrTbrArgVe TACACCAGGGT 1850 AGCCAAGGCTN 1470 AGAGAGACAGAM 1590 AGGCAGAGGCAA | 1000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | pSergleuHet1 cocccrgarge 1130 pSerglyGlyl cagragage 1250 rzlleGluTrp carcagage 1370 retocracae 1490 agacrgaegga 1610 | +31 ThrG1nAspCy ACCCAGGACTG 1140 +35 ProHisAlsTr CCACATGCCAC 1260 +35 LeuGlnLysLa CTGCAAAAGC 1380 CAAATCCCAT 1500 GAGACTCTGA | yaleuGinGin jaleuGinGin jactteCAGCAG 1150 50 hrHisTyrArj cocactaccad 1270 90 sulletArgSer tCATGCGCTC 1390 ATATTCTTCT 1510 | Serarglys TCACCGAAG 1160 GlyThrTrp GGCACCTGG 1280 rGluProArg AGAGCCACCC 1400 CCACTTAATC 1520 AGAGACTCAC | ValGlyAapSe GTGGGAGACTC 1170 *36 TyrLeuThrGl TACCTGACGGC 1290 *46 ProGlyValLe CCAGGAGTCC 1410 CGGGTAGAGGAC 1530 AAGAGACTCCA 1650 | O IPPTOASSILIO IPP | aThrGluTyrii CACGGAGTACA 1190 rTrpGlyGlnG CTGGGGCCAGG 1210 +406 aProPhaProc CCCATTTCCC 1430 .GGGAGGGAGA 1550 .AGACTAATAG | TETTCTET 1200 ELYCYALIA GCTGGGGA 1220 FAGCOCAGC 1440 ECTGGGGAG 1560 AGACACAGA 1680 |
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| •290 ArgGlyAlaThr CGTEGCECCACG 1090 •330 AleGlyTyrSer GCCGGCTACTCG 1210 •370 ThrValGlyHis ACCGTEGCCAC 1330 AGCCTEGCCAC 1450 GCAGACAGAGAC 1570 GATGGAATAGAC 1690 GCCCCACCTGG 1810 ATATGCACACA | AleleuGlui GCCCTEGAGG 1100 AmpGlySeri GATGGCAGG 1220 APheGlyVel: CTTTGGGTG 1840 CAGAAACAGA 1460 CAGAAACAGA 1580 AAAGATGAGA 1700 ACGTGATCTG 1820 | 990 +30 Leullet Valle CTCATGGTOCT 1110 +34 LyaAspSerCy AAGGACTOCTG 1230 +38 TyrThrArgVe TACACCAGGGT 1850 AGGCAAGGCTT 1470 AGGCAGAGGCA 1590 AGGCAGAGGCA 1710 GCTGGCCCTCA 1830 ACACACAGATG | 1000 0 10AnDValPr CAACGTGCC 1120 0 12LysGlyAs CAAGGGGGA 1240 10 11SerGlnTy CCCCACTA 1360 CACAGAGAGT 1600 GACAGGGGGT 1720 GGCTGCTGC 1840 GTCACACAG | ADIO CARGLOUNCT CARGEORY AND | +31 ThrG1nAspCy ACCCAGGACTE 1140 +32 ProHisAlar CCACATGCCAC 1260 +37 LeuG1nLyala CTGCAAAAGC 1380 CAAATCCCAT 1500 GAGACTCTGA 1620 GCAGGGGGAGT 1740 TTGCTGGAGAC 1860 ACACACCGATG | yalauGinGin yalauGin yal | Serarglys TCACCGAAG 1160 G1yThrTrp GGCACGTGG 1280 F61uProArg LGAGCCACGC 1400 CCAGTTAATC 1520 ACAGACTCAI 1640 TCCTGGAGGG 1760 TGAACACAC 1880 | ValGlyAspSe GTGGGAGACTC 1170 -38 TyrLsuThrGl TACCTGACGG 1290 -40 IPPOGLYValLe CCAGGAGTCC 1410 CCGGTAGAGGA 1530 AAGAGACTCCA 1650 CAGACAGCCCA 1770 ATGGATGCACA 1890 | O IPPROASENTIO INCOMANTATION 1180 IO | aThrGluTyric caccgagataca 1190 rTrpGlyGlnd cTGGGGCCAGG 1810 +406 aProPhaPro cCCATTTCCC 1430 aCGGAGGGAGA 1550 aGGACTAATAG 1670 aCTTACCTCCC 1790 aCCCAATGCACA | TETTCET 1200 ELYCYALIA GECTEGECA 1220 ELAGOCCASC 1440 EGCTEGECAG 1560 AGACACAGA 1680 TTCAGCCAA 1800 CACACAGAG 1920 |
| •290 ArgGlyAleThr CGTEGCGCCACG 1090 •330 AleGlyTyrSer GCCGGCTACTCG 1210 •370 ThrValGlyBis ACCGTGGGCCAC 1330 AGCCCTGGCCTC 1450 GGAGACAGAGAC 1570 GATGGAATAGAC 1690 GCCCCACCTGC 1810 ATATGCACACA 1930 | AleleuGlui GCCCTGAGG 1100 AmpGlySeri GATGGCAGC 1220 APheGlyVal CTTGGGGTG 1840 CTGAGAGAA 1460 CAGAAACAGA 1700 ACGTGATCTG 1820 CACGGATGC 1940 | 990 +90 LeuHetValle CTCATGGTCCT 1110 +34 LyaAspSerCy AAGGACTCCTG 1230 +32 TyrThrArgVo TACACCAGGCT 1350 AGGCAAGGCTCA 1470 AGGCAGAGCAA 1590 AGGCAGAGGCAA 1710 GCTGGCCCTCA 1830 ACACACAGATG 1950 | 1000 0 10AssValPricascore 1120 0 1120 0 1120 10 11SerGlnTy 10TroccaGTa 1360 1260 1260 1260 1260 1260 12720 1360 1360 1360 1360 1360 1360 1360 136 | pSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG | +31 ThrG1nAspCy ACCCAGGACTG 1140 +35 ProHisAlsTr CCACATGCCAC 1260 +35 LeuGlnLysLa CTGCAAAAGC 1380 CAAATCCCAT 1500 GAGACTCTGA 1620 GCAGGGGGAGT 1740 TTGCTGGAGAC 1860 ACACACCGATG | paleuginginginginginginginginginginginginging | Serarglys TCACCGAAG 1160 GlyThrTrp GGCACCTGG 1280 rGluProArg AGAGCCACCC 1400 CCAGTTAATC 1520 ACACACTCAC 1640 TCCTGGAGGG 1760 TGAACACAC 1880 TAGAGATATT 2000 | ValGlyAspSe GTGGGAGACTC 1170 *36 TyrLeuThrGl TACCTGACGGC 1290 *46 ProGlyValLe CCAGGAGTCC 1410 CGGGTAGAGGAC 1530 AAGAGACTCCA 1650 CAGACAGCCCA 1770 ATGGATGCACA 1890 GCACACACAGA 2010 | O IPPTOASSILIO IPP | aThrGluTyrii caccgagtaca 1190 rTrpGlyGlnG cTGGGGCCAGG 1210 +406 aProPhaProc cccatttccc 1430 aGGGAGGGAGA 1550 caccgaggaggaga 1550 cactgaggaggaga 1570 ccttacctccc 1790 agccaatgcaca 1910 agatatacaca 2030 | TETPLETY TETTCTET 1200 ELYCYALIE GCTGGGCA 1220 EAGCOCAGC 1440 ECTGGGCAG 1560 AGACACAGA 1680 TTCAGCCAA 1800 CACACAGAG 1920 TGGATGCAC 2040 |
| •290 ArgGlyAleThr GGTEGCECACG 1090 •330 AleGlyTyrSer GCCGGCTACTCG 1210 •370 ThrValGlyHis ACCGTGGCCAC 1330 AGCCCTGGCCTC 1450 GGAGACAGAGAC 1570 GATGGAATAGAC 1690 GCCCCACCTGG 1810 ATATGCACACA 1930 GCACATGCCAA | AlelauGlui GCCCTGAGG 1100 AmpGlySari GATGGCAGG 1220 ApheGlyVel: CTTTGGGTE 1940 CAGAAACAGA 1580 AAAGATGAGA 1700 ACGTGATCTE 1820 CACGGATGC 1940 TGCACGCAC | 990 +30 Leullet Valle CTCATGGTCT 1110 +34 LyeAspSercy AAGGACTCCTG 1230 +32 TyrThrArgve TACACCAGGGT 1850 AGGCAAGGCTC 1470 AGGCAGAGACAGA 1710 AGCCAGGCCTCA 1830 ACACACAGATG 1950 ACACACAGATG 1950 ACATCAGTGCA | 1000 0 0 0 0 0 0 0 0 0 0 1120 0 0 1240 0 0 113erGlnTy 0 0 113erGlnTy 0 0 0 115erGlnTy 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | ADIO OARGLOUNOTI COCGCTGATGI 1180 PSOTGLYGLY CAGTGGAGGC 1250 TILOGLUTEPI CATOCAGTGG 1370 TOTOCTGGCAC 1490 AGACTGAGGGG 1730 TCTGCCTTCAT 1850 AGATACGCAA/ 1970 ACAGAGAGATATC | +31 ThrG1nAspCy ACCCAGGACTE 1140 +32 ProHisAlsTi CCACATGCCAC 1250 -32 LeuGlnLysLi CTGCAAAAGC 1380 CAAATCCCAT 1500 GAGACTCTGA 1620 GCCAGGGGAGT 1740 TTGCTGGAGAC 1860 ACACACCGATG 1980 GCACACACCGATG 1980 | ATGTTGCGCACA | Serarglys TCACCGAAG 1160 G1yThrTrp GGCACCTGG 1280 G1uProarg AGACCCACCC 1400 GCAGTTAATC 1520 AGACACTCAI 1640 TCCTGGAGG 1760 TGAACACAC 1880 TAGAGATAT 2000 CACAGATAT | ValGlyAspSe GTGGGAGACTC 1170 *36 TYPLSUTHTG1 TACCTGACGGG 1290 *46 PPTGGIYVS16 CCAGGAGTCC 1410 CCAGGAGTCC 1430 AAGAGACTCCA 1630 CAGACAGCCCA 1770 ATGGATGCACA 1890 GCACACACACAC GCACACACACACAC GCACACACA | O IPPTOASSILIO IPP | aThrGluTyrii caccgagtaca 1190 rTrpGlyGlnG cTGGGGCCAGG 1210 +406 aProPhaProc cccatttccc 1430 aGGGAGGGAGA 1550 caccgaggaggaga 1550 cactgaggaggaga 1570 ccttacctccc 1790 agccaatgcaca 1910 agatatacaca 2030 | TETPLETY TETTCTET 1200 ELYCYALIE GCTGGGCA 1220 EAGCOCAGC 1440 ECTGGGCAG 1560 AGACACAGA 1680 TTCAGCCAA 1800 CACACAGAG 1920 TGGATGCAC 2040 |
| •290 ArgGlyAlaThr CGTEGCECCACG 1090 •330 AleGlyTyrSer GCCGCTACTCG 1210 •370 ThrValGlyHis ACCCTEGCCAC 1330 AGCCTEGCCAC 1450 GCAGACAGAGAC 1570 GATGGAATAGAC 1690 GCCCCACCTGG 1810 ATATGCACACA 1930 GCACATGCCAA 2050 | #80 AleleuGlui GCCTTGAGG 1100 AmpGlySeri GATGGCAGG 1220 #PheGlyVel: TTTTGGGTG 1840 CAGAAACAGA 1580 AAAGATGAGA 1700 ACGTGATCTG 1820 CACGGATGC 1940 TGCACGCACC 2060 | +990 +90 Leullet Valle CTCATGGTCT 1110 +94 LyaAspSerCy AAGGACTCCTG 1230 +38 TyrTbrArgVe TACACCAGGGT 1850 AGGCAAGGCTA 1590 AGGCAGAGGCA 1710 GCTGGCCCTCA 1830 ACACACAGATG 1950 ACATCAGTGCA 2070 | MARRYAIPTCAACGTGCC 1120 0 121, yaGlyAs CAAGGGGGA 1240 10 11360 11360 11480 114 | pSergleuHet1 cocccrrator 1180 pSerglyGlyl cagragagaga 1250 rc1leGluTrpl carcagagaga 1370 retocracaga 1610 rcgacagagaga 1610 rctgacagagaga 1730 rcttgactraa 1850 agataagaga 1970 acagagagataa | +31 ThrG1nAspCy ACCCAGGACTE 1140 +32 ProHisAlsTi CCACATGCCAC 1260 -39 LeuGlnLysLi CTGCAAAAGC 1380 CAAATCCCAT 1500 GAGACTCTGA 1620 GCCAGGGGAGT 1740 TTGCTGGAGAC 1860 ACACACCGATG 1980 GCACACACCGATG 1980 GCACACACCGATG 2100 | ATATTCTTCT 1750 CCACACGCAC 1630 ATATTCTTCT 1750 CCACACGCAC 1630 CCACACGCAC 1670 CCACACGCAC 1790 CACACGCAC 2110 | Serarglys TCACCGAAG 1160 G1yThrTrp GGCACCTGG 1280 G1uProarg AGACCACCC 1400 GCAGTTAATC 1520 ACACACTCAI 1640 TCCTGGAGG 1760 TGAACACAC 1880 TAGAGATAT 2000 CACAGATAT 2120 | ValGlyAspSe GTGGGAGACTC 1170 *36 TyrLeuThrG1 TACCTGACGGG 1290 *46 PTGGIyValLe PCCAGGAGTCC 1410 CCAGGAGACTCCA 1530 AAGAGACTCCA 1650 CAGACAGCCCA 1770 ATGGATGCACA 1890 GCACACACACAGA 2010 GCACACACACATC 2130 | O IPPROACTION OF THE PROACTION OF THE PR | aThrGluTyric CACGGGCTACA 1190 rTrpGlyGlnG CTGGGGCCAGG 1810 +406 aProPhaPro CCCATTTCCC 1430 AGGGAGGGAGAI 1550 AGGGAGGAGAI 1550 AGGCTAATAG 1670 CCTTACCTCCC 1790 AGGATGACA 2030 | TETTCTET 1200 ELYCYALIA ECCTECECA 1220 ELACOCASC 1440 ECCTECECASC 1560 ECCTECECASC 2160 |
| •290 ArgGlyAleThr GGTEGCECACG 1090 •330 AleGlyTyrSer GCCGGCTACTCG 1210 •370 ThrValGlyHis ACCGTGGCCAC 1330 AGCCCTGGCCTC 1450 GGAGACAGAGAC 1570 GATGGAATAGAC 1690 GCCCCACCTGG 1810 ATATGCACACA 1930 GCACATGCCAA | AleleuGlui GCCTTGAGG 1100 AmpGlySeri GATGGCAGC 1220 APheGlyVel TTTGGGGTG 1840 CTGAGAGAAA 1460 CAGAAACAGA 1700 ACGTGATCTG 1820 CACGGATGC 1940 TGCACGCAC 2060 | 990 +90 LeuHetValle CTCATGGTCCT 1110 +34 LyaAspSerCy AAGGACTCCTG 1230 +32 TyrThrArgW TACACCAGGGT 1350 AGGCAGAGGCT 1470 AGGCAGAGACAGAI 1590 AGGCAGAGGCAI 1710 CCTGGCCCTCA 1830 ACACACAGATG 1950 ACACACAGATG 2070 GATGCACACAC | 1000 0 10ARDVAIPT CARCETECC 1120 0 12120 10 11SerGINTy CARCEGEA 1240 10 11SerGINTy CTCCCAGTA 1360 16CGTCGAACT 1480 16ACAGAGAGAG 1720 1720 1720 1720 1720 1720 1720 1720 | ADIO OARGLOUHOTI COSSCTGATGI 1180 PSOTGLYGLYGLY CAGTGGAGGC 1250 TILOGLUTES LATTO TOTOCTAGCAC 1490 ACACTGACGGA 1610 TCTGCCTTCAT 1850 AGATACGCAAA 1970 ACAGAGATATC 2090 CACACCGATGA | +31 ThrG1nAspCy ACCCAGGACTE 1140 +35 ProHisAlsTi CCACATGCCAC 1260 +35 LeuGinLysL CTGCAAAAGC 1380 CAAATCCCAT 1500 GAGACTCTGA 1620 GCAGGGGAGT 1740 TTGCTGGAGAC 1860 ACACACCGATE 1980 GCACACACCGATE CTGACTCCATC | paleuGinGin paleuGinGin paleuGinGin paleuGinGin parining | Serarglys TCACCGAAG 1160 G1yThrTrp GGCACGTGG 1280 F61uProArg MGAGCCACCC 1400 FCAGTTAATC 1520 AGAGACTCAI 1640 TCCTGGAGGG 1760 TGAACACAC 1880 TAGAGATAT 2000 CACAGATAT 2120 TCTGAAGGC | ValGlyAspSe GTGGGAGACTC 1170 -38 TyrLsuThrGl TACCTGACGC 1290 -40 IPROGLYValLa CCAGGAGTCC 1410 CCAGGAGTCC 1430 AGAGACACCAC 1890 GCACACACACA 2010 GCACACACACAT 2130 GGTTGTTTAGC | O IPPROASENTIO IPPROASENTIO INCOCAMATATO 1180 IO IPPROASENTION IO IPPROASENTION INCOME | aThrGluTyric CACGGGCTACA 1190 rTrpGlyGlnG CTGGGGCCAGG 1810 +406 aProPhaPro CCCATTTCCC 1430 AGGGAGGGAGAI 1550 AGGGAGGAGAI 1550 AGGCTAATAG 1670 CCTTACCTCCC 1790 AGGATGACA 2030 | TETTCTET 1200 ELYCYALIA ECCTECECA 1220 ELACOCASC 1440 ECCTECECASC 1560 ECCTECECASC 2160 |
| •290 ArgGlyAleThr GGTEGCECCACG 1090 •330 AleGlyTyrSer GCCGGCTACTCG 1210 •370 ThrValGlyHis ACCGTGGCCAC 1330 AGCCCTGGCCTC 1450 GGAGACAGAGAC 1570 GATGGAATAGAC 1690 GCCCCACCTGC 1810 ATATGCACACA 1930 GCACATGCCAA 2050 CACACCGATGT 2170 | AleleuGlui GCCTTGAGG 1100 AspGlySari GATGGCAGC 1220 ApheGlyVell TITTGGGTE 1340 CAGAAACAGA 1580 AAAGATGAGA 1700 ACGTGATCTE 1820 CACGGATGCI 1940 TGCACGCACA 2060 | +990 +90 LeulletValle CTCATGGTCT 1110 +94 LyaAspSerCott 1230 +92 TyrThrArgwi TACACCAGGGT 1850 AGGCAAGGCTC 1470 AGGCAGAGGCAI 1710 AGGCAGAGGCAI 1710 AGCCAGAGGCAI 1790 ACACACAGATG 1990 ACATCAGTGCA 2070 GATGCACACACA | MARRYALPET CARCETECC 1120 0 12120 0 12120 10 11SerGlaty 1240 10 11SerGlaty 1360 11SerGlaty 1480 16CETCEACAC 1480 1720 1720 1720 1720 1720 1720 1720 172 | ADIO OARGLOUNOTI COGGCTGATGI 1180 PSOTGLYGLYGLY CAGTGGAGGC 1250 TILOGLUTEPI CATCGAGTGG 1370 TETCCTGGCAC 1490 AGACTGAGGGG 1730 TCTGCCTTCAT 1850 AGATACGCAAA 1970 ACAGGAGATATC 2090 CACACCGATGG 2210 | +31 ThrG1nAspCy ACCCAGGACTE 1140 +35 ProHisAleTE CCACATGCCAC 1260 +35 LeuG1nLysL CTGCAAAAGC 1380 CAAATCCCAT 1300 GAGACTCTGA 1620 GCAGGGGAGT 1740 TTGCTGGAGAC 1860 ACACACCGATG 1980 GCACACACCGATG 1980 GCACACACCGATG 1980 CTGACTCCATC 2100 CTGACTCCATC 2220 | paleuGinGin paleuGinGin paleuGinGin paleuGinGin pariningin parinin | Serarglys TCACCGAAG 1160 G1yThrTrp GGCACGTGG 1280 F61uProArg MGAGCCACCC 1400 FCAGTTAATC 1520 AGAGACTCAI 1640 TCCTGGAGGG 1760 TGAACACAC 1880 TAGAGATAT 2000 CACAGATAT 2120 TCTGAAGGC 2240 | ValGlyAspSe GTGGGAGACTC 1170 -36 TyrLeuThrGl TACCTGACGG 1290 -40 IPROGLYValLe CCAGGAGTCC 1410 CCGGTAGAGGAC 1530 AAGAGACTCCA 1650 CAGACAGCACA 1890 GCACACACAGA 2010 GCACACACACA 2130 GGTTGTTTAGG 2230 | O IPPTOASSILO IPPT | aThirGluTyrii caccgagataca 1190 rTrpGlyGlnd cTGGGGCCAGG 1310 -406 aProPhaPro cCCATTTCCC 1430 aGGGAGGAGAG 1550 aGGCAGGAGAGAC 1570 aCCTTACCTCCC 1790 aGCCAATGCACA 1910 aGATATACACA 2030 aCACACACACCAA 2150 TCTGGTTCTTA 2270 | TETPLET 1200 CIPCYALLE GETEGGEA 1220 CIPCYALLE GETEGGEAG 1360 CIPCGGEAG 1360 CIPCGGEAG 1360 CIPCGGEAG 1920 CIPC |
| •290 ArgGlyAleThr GGTEGCECCACG 1090 •330 AleGlyTyrSer GCCGGCTACTCG 1210 •370 ThrValGlyHis ACCGTGGCCAC 1330 AGCCCTGGCCTC 1450 GGAGACAGAGAC 1570 GATGGAATAGAC 1690 GCCCCACCTGC 1810 ATATGCACACA 1930 GCACATGCCAA 2050 CACACCGATGT 2170 | AleleuGlui GCCTTGAGG 1100 AspGlySari GATGGCAGC 1220 ApheGlyVell TITTGGGTE 1340 CAGAAACAGA 1580 AAAGATGAGA 1700 ACGTGATCTE 1820 CACGGATGCI 1940 TGCACGCACA 2060 | +990 +90 LeulletValle CTCATGGTCT 1110 +94 LyaAspSerCott 1230 +92 TyrThrArgwi TACACCAGGGT 1850 AGGCAAGGCTC 1470 AGGCAGAGGCAI 1710 AGGCAGAGGCAI 1710 AGCCAGAGGCAI 1790 ACACACAGATG 1990 ACATCAGTGCA 2070 GATGCACACACA | MARRYAIPTCAACGTGCC 1120 0 124, yaGlyAs CAAGGGGGA 1240 10 135erGlnTy CTCCCAGTA 1360 6GGTCGAACT 1480 6ACAGGAGAG 1600 6ACAGGGGGC 1720 6GCTGCTGC 1840 6TCACACAG 1960 CACGGATGC 2080 CAGGATGCACA 2200 CCATGCATGC | ADIO OARGLOUNOTI COCGCTGATGI 1130 PSOTGLYGLYGLY CAGTGGAGGC 1250 TILOGLUTEP CATCGAGGG 1370 RETOCTGGCAC 1490 RGACTGAGGGA 1610 TGGACAGAGGG 1730 TCTGCCTTCAT 1850 AGATACGCAAI 1970 ACAGAGATATC 2090 CACACCGATGA 2210 TTGCCGAATGC | +31 ThrG1nAspCy ACCCAGGACTE 1140 +32 ProHisAl=CT CCACATGCCAC 1260 -39 LeuGInLysLL CTGCAAAAGC 1280 CAAATCCCAT 1500 GAGACTCTGA 1620 CCAGGGGGAGT 1740 TTGCTGGAGAC 1860 ACACACCGATG 1980 GCACACACCGATG 1980 CCACACACCGATG 1220 CCCCCAAACTCT CCCCCAAACTCT CCCCCCCCCC | ATCTTCCCCCAAATI | Serarglye TCACCGAAG 1160 GlyThrTrp GGCACCTGG 1280 GluProArg AGAGCCACCC 1400 CCAGTTAATC 1520 ACACACTCAC 1640 TCACACACAC 1680 TAGAGATAT 2000 CCACAGATAT 2120 TCTGAAGGC 2240 CTATTTCTCC | ValGlyAspSe GTGGGAGACTC 1170 *36 TyrLeuThrGl TACCTGACGGG 1290 *46 ProGlyValLe CCAGGAGTCC 1410 CGGGTAGAGGAC 1530 AAGAGACTCCA 1650 CAGACAGCACA 1770 ATGGATGCACA 1890 GCACACACAGA 2010 GCACACACAGA 2010 GCACACACATC 2130 CGTTGTTTAGC 2250 | O IPPTOASSILO IPPT | aThirGluTyrii caccgagataca 1190 rTrpGlyGlnd cTGGGGCCAGG 1310 -406 aProPhaPro cCCATTTCCC 1430 aGGGAGGAGAG 1550 aGGCAGGAGAGAC 1570 aCCTTACCTCCC 1790 aGCCAATGCACA 1910 aGATATACACA 2030 aCACACACACCAA 2150 TCTGGTTCTTA 2270 | TETPLET 1200 CIPCYALLE GETEGGEA 1220 CIPCYALLE GETEGGEAG 1360 CIPCGGEAG 1360 CIPCGGEAG 1360 CIPCGGEAG 1920 CIPC |
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FACTOR VII

FACTOR IX

FACTOR X

PROTHROMBIN

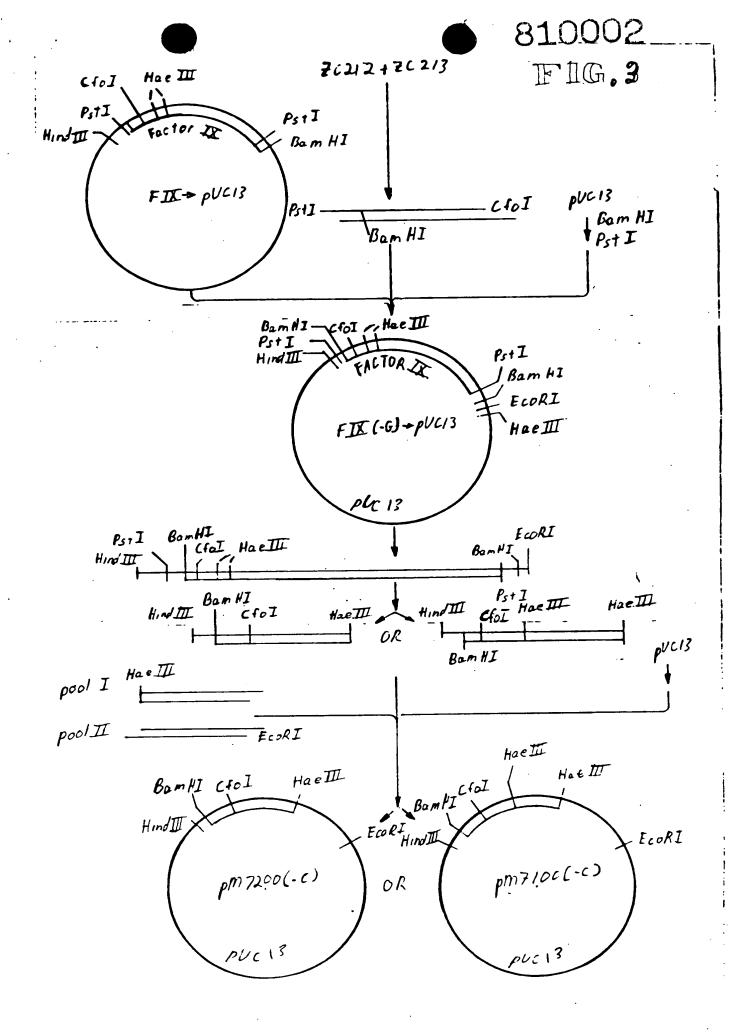
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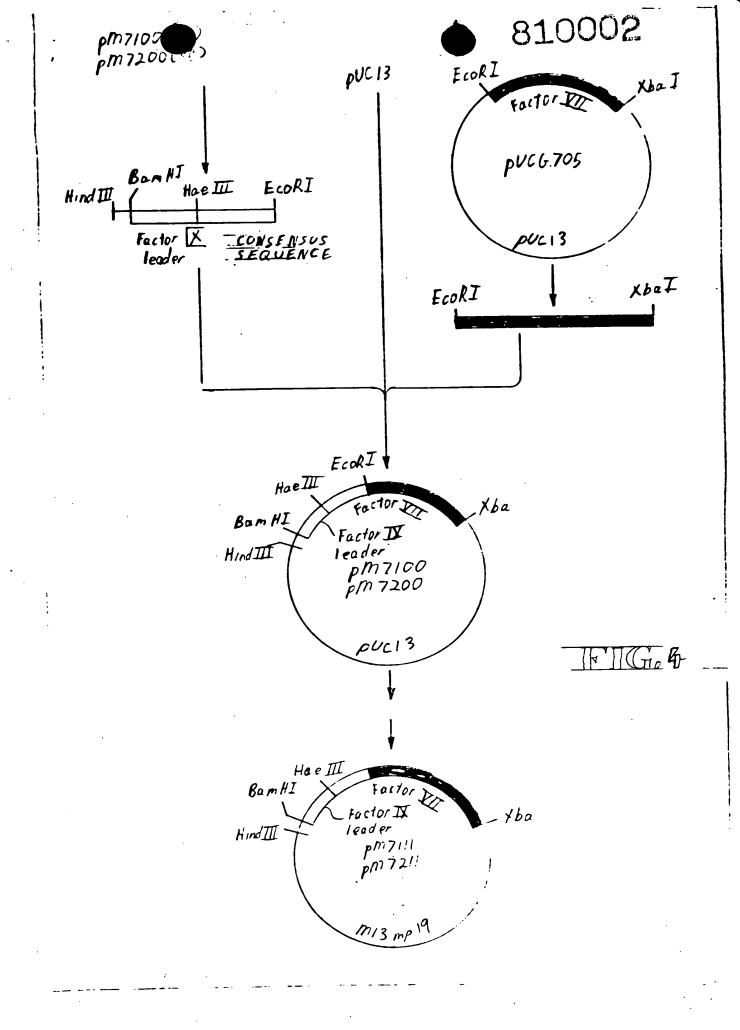
FACTOR VII

FACTOR IX

FACTOR X

PROTEIN C





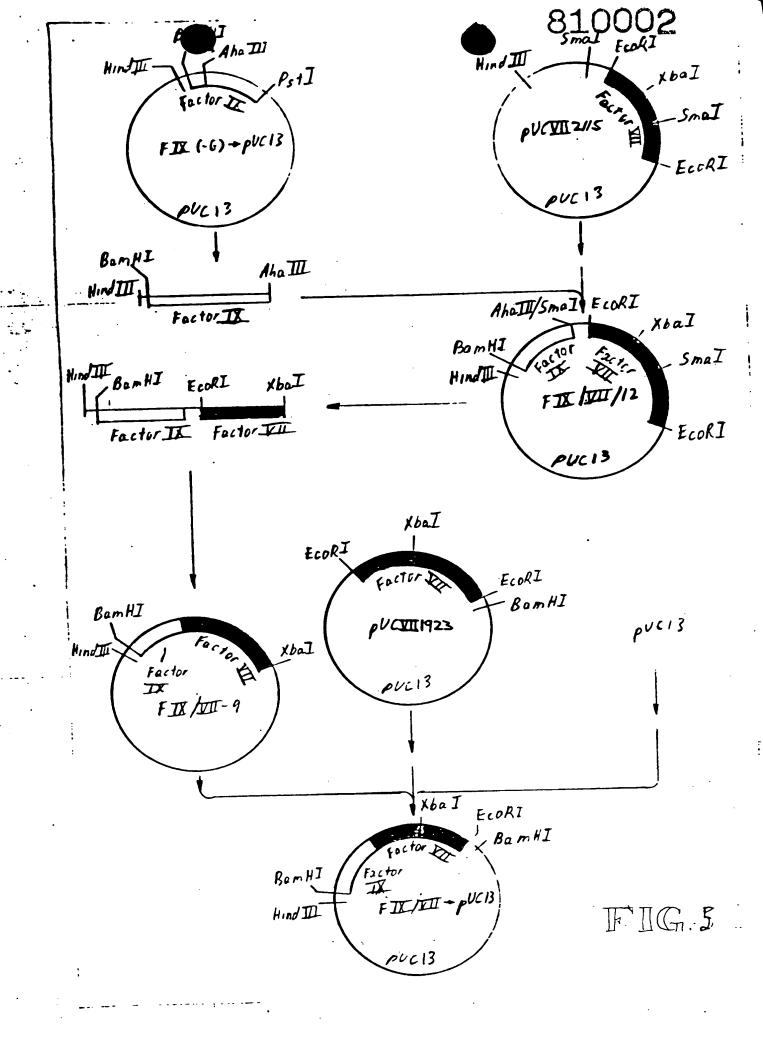
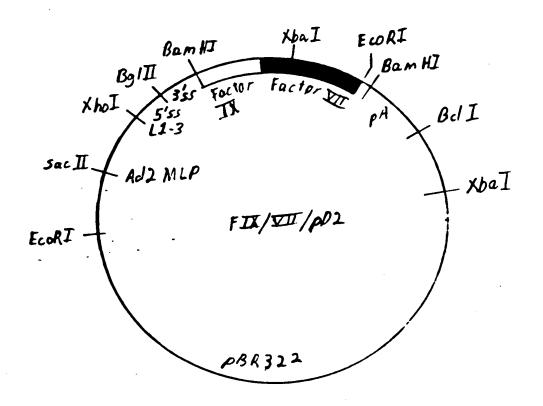


FIG.6



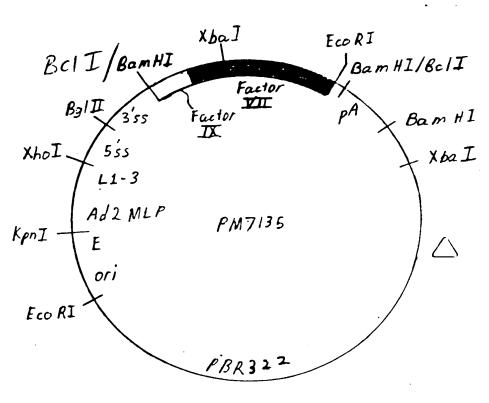


FIG.8

FIGURE 7

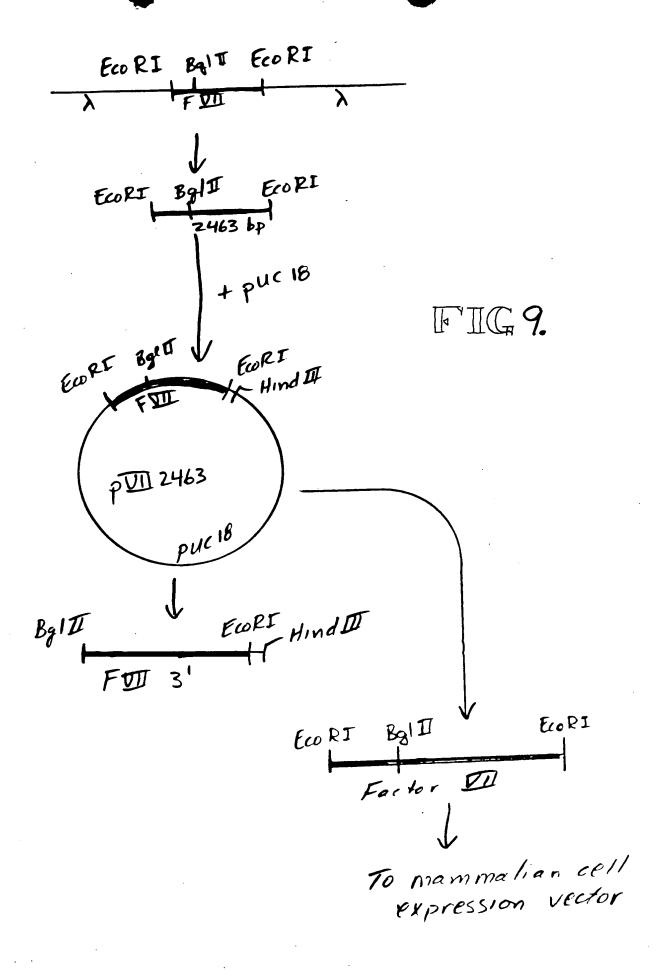
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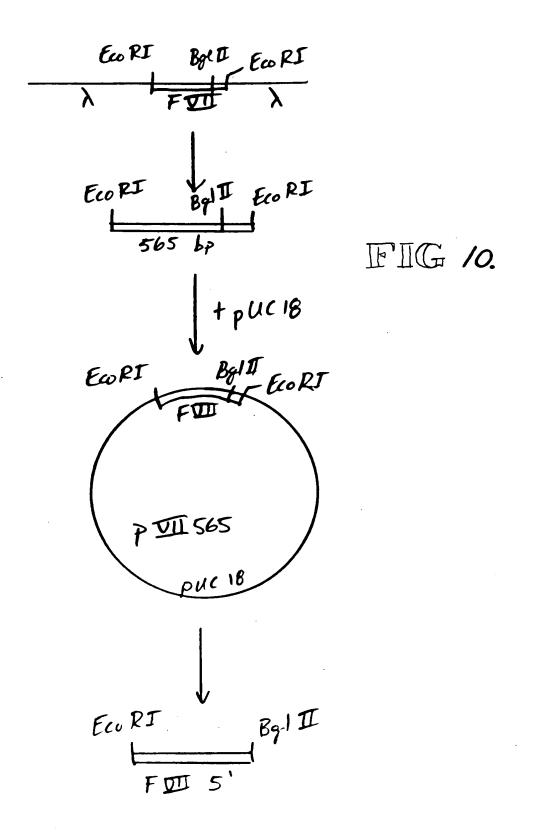
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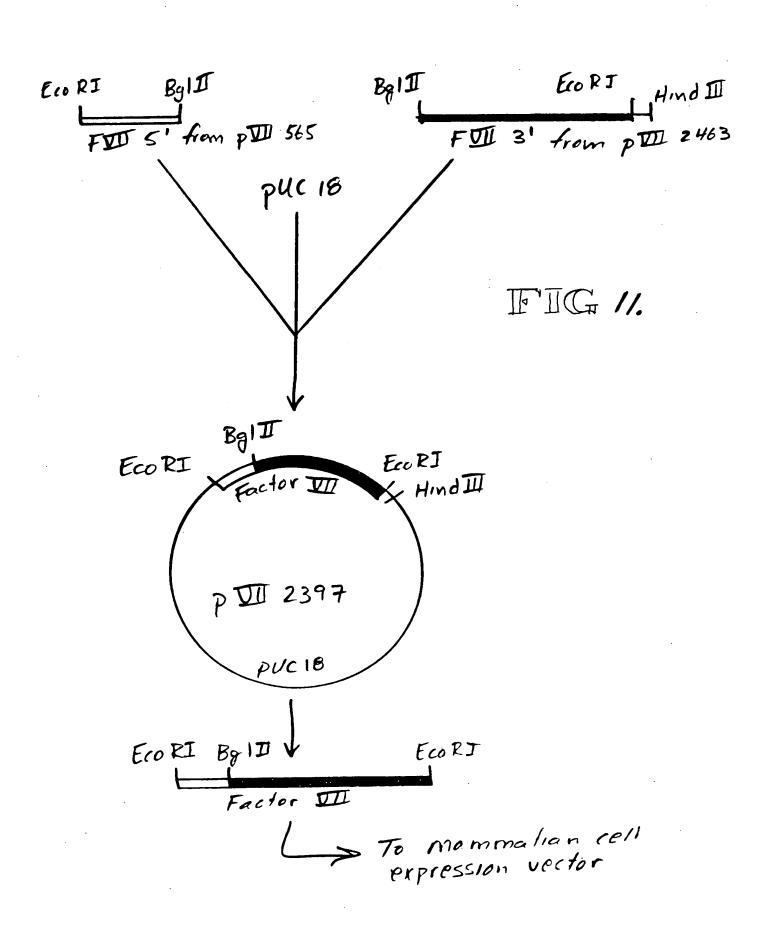
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1958 1968 1978 1988 1998 ACACAGATAT ACACATGGAG TGCACGCACA TGCCAATGCA CGCACACATC 2018 2028 2038 2048 2008 AGTGCACACG GATGCACAGA GATATGCACA CACCGATGTG CGCACACACA 2068 2078 2088 2058 GATATGCACA CACATGGATG AGCACACACA CACCAAGTGC GCACACACAC 2108 2118 2128 2138 2148 CGATGTACAC ACAGATGCAC ACACAGATGC ACACACCCG ATGCTGACTC 2158 2168 2178 2188 2198 CATGTGTGCT GTCCTCTGAA GGCGGTTGTT TAGCTCTCAC TTTTCTGGTT 2208 2218 2228 2238 2248 CTTATCCATT ATCATCTTCA CTTCAGACAA TTCAGAAGCA TCACCATGCA 2258 2268 2278 2288 TGGTGGCGAA TGCCCCCAAA CTCTCCCCCA AATGTATTTC TCCCTTCGC1 2308 2318 2328 2338 2348 GGGTGCCGGG CTGCACAGAC TATTCCCCAC CTGCTTCCCA GCTTCACAAT 2358 2368 2378 2388 2398 2408 2418 2428 2438

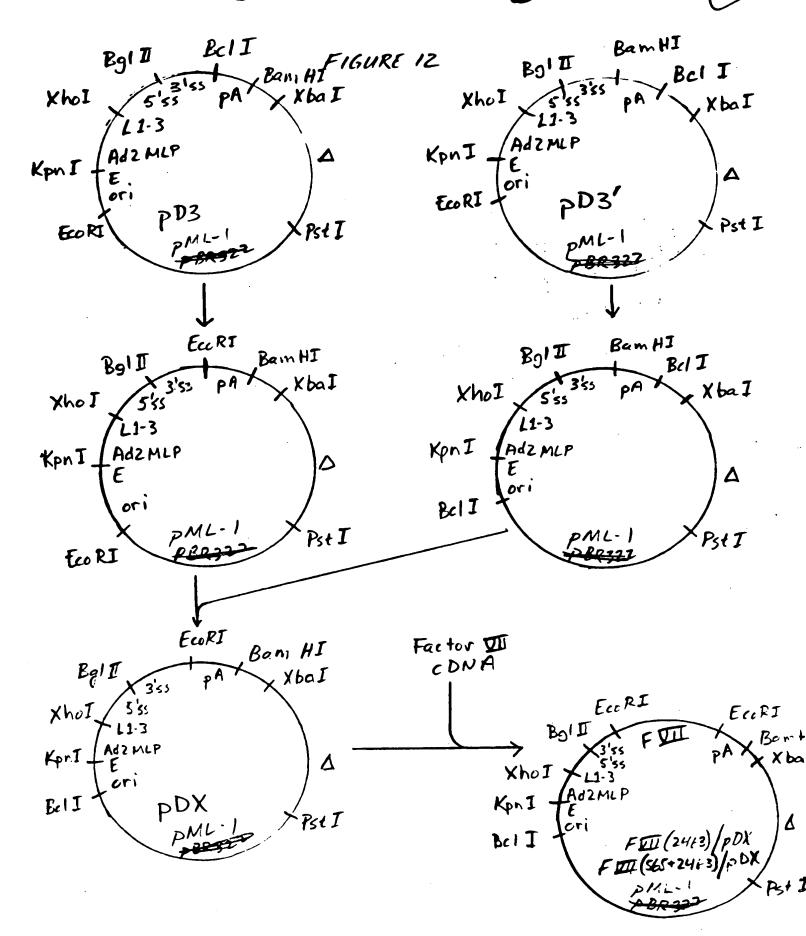
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1568 1578 1588 1598 1608 1618 1628
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1638 1648 1658 1668 1678 1688 1698
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1708 1718 1728 1738 1748 1758 1768
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1778 1788 1798 1808 1818 1828 1838
GATGCACAGA GATATGCACA CACCGATGTG CGCACACACA GATATGCACA CACATGGATG AGCACACACA

1848 1858 1868 1878 1888 1898 1908
CACCAAGTGC GCACACACA CGATGTACAC ACAGATGCA ACACAGATGC ACACACACC ATGCTGACTC

1918 1928 1938 1948 1958 1968 1978 CATGTGTGCT GTCCTCTGAA GGCGGTTGTT TAGCTCTCAC TTTTCTGGTT CTTATCCATT ATCATCTTCA

1988 1998 2008 2018 2028 2038 2048
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2058 2068 2078 2088 2098 2108 2118
TCCCTTCGCT GGGTGCCGGG CTGCACAGAC TATTCCCCAC CTGCTTCCCA GCTTCACAAT AAACGGCTGC